

RAW SEQUENCE LISTING

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Application Serial Number: 10/528,460
Source: PCT
Date Processed by STIC: 3-29-05

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DATE: 03/29/2005

PATENT APPLICATION: US/10/528,460

TIME: 15:25:49

Input Set : A:\LeA 36 282.ST25.txt

Output Set: N:\CRF4\03292005\J528460.raw

3 <110> APPLICANT: Bayer HealthCare AG
 4 Golz, Stefan
 5 Bruggemeier, Ulf
 6 Geerts, Andreas
 8 <120> TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
 Human
 9 Phosphodiesterase 11A (PDE11A)
 11 <130> FILE REFERENCE: LeA 36 282
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/528,460
 C--> 13 <141> CURRENT FILING DATE: 2005-03-18
 13 <150> PRIOR APPLICATION NUMBER: EP02021365.8
 14 <151> PRIOR FILING DATE: 2002-09-24
 16 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/010376
 17 <151> PRIOR FILING DATE: 2003-09-18
 19 <160> NUMBER OF SEQ ID NOS: 5
 21 <170> SOFTWARE: PatentIn version 3.3
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1784
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1
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 33 gtgggtgaaat ttaccaaata ctttgaattg atgtcccaaa agtgcagtgct tgatgctgag 180
 35 aacagtttca aagaaagcat ggagaaatca tcataactccg actgggctaataaataacagc 240
 37 attgctgagc tggttgcttc aacaggcctt ccagtgaaaca tcagtgatgc ctaccaggat 300
 39 ccgcgctttg atgcagaggc agaccagata tctgggtttc acataagatc tgttctttgt 360
 41 gtccctattt ggaatagcaa ccaccaaata attggagtgg ctcaagtgtt aaacagactt 420
 43 gatgggaaac cttttgatga tgcagatcaa cgactttttg aggcttttgt catcttttgt 480
 45 ggacttggca tcaacaacac aattatgtat gatcaagtga agaagtcctg ggccaagcag 540
 47 tctgtggctc ttgatgtgct atcataccat gcaacatgtt caaaagctga agttgacaag 600
 49 ttaaggcag ccaacatccc tctggtgtca gaacttgcca tcgatgacat tcattttgat 660
 51 gacttttctc tcgacgttga tgccatgatc acagctgctc tccggatgtt catggagctg 720
 53 gggatgttac agaaatttaa aattgactat gagacactgt gtaggtggct tttgacagtg 780
 55 aggaaaaact atcggtatgt tctataccac aactggagac atgccttcaa cgtgtgtcag 840
 57 ctgatgttcg cgatgttaac cactgctggg tttcaagaca ttctgaccga ggtggaaatt 900
 59 tttagcgtga ttgtgggatg cctgtgtcat gacctcgacc acaggggaac caacaatgcc 960
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 63 catcaccatt tcaaccacgc cgtgatgatc cttcaaagtg agggtcacaa tatctttgct 1080
 65 aacctgtcct ccaaggaata tagtgacctt atgcagcttt tgaagcagtc aatattggca 1140
 67 acagacctca cgctgtactt tgagaggaga actgaattct ttgaacttgt cagttaaagga 1200
 69 gaatacgatt ggaacatcaa aaaccatcgt gatatatctc gatcaatgtt aatgacagcc 1260
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 73 accagtgagt tcttcgaaca aggagatcgg gagagattag agctcaaaact cactccttca 1380

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75 gcaatttttg atcggaaccg gaaggatgaa ctgcctcggt tgcaactgga gtggattgat 1440
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79 ctagattcag tagctacaaa cagaagtaag tgggaagagc tacacaaaaa acgactgctg 1560
81 gcctcaactg cctcatcctc ctccccctgcc agtggttatgg tagccaagga agacaggaac 1620
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85 cagcaatgtc atccttttgt tcttttagct cagaaagacc taacatctca aggatgcact 1740
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102 20 25 30
105 Glu Leu Val Ala Ser Thr Gly Leu Pro Val Asn Ile Ser Asp Ala Tyr
106 35 40 45
109 Gln Asp Pro Arg Phe Asp Ala Glu Ala Asp Gln Ile Ser Gly Phe His
110 50 55 60
113 Ile Arg Ser Val Leu Cys Val Pro Ile Trp Asn Ser Asn His Gln Ile
114 65 70 75 80
117 Ile Gly Val Ala Gln Val Leu Asn Arg Leu Asp Gly Lys Pro Phe Asp
118 85 90 95
121 Asp Ala Asp Gln Arg Leu Phe Glu Ala Phe Val Ile Phe Cys Gly Leu
122 100 105 110
125 Gly Ile Asn Asn Thr Ile Met Tyr Asp Gln Val Lys Lys Ser Trp Ala
126 115 120 125
129 Lys Gln Ser Val Ala Leu Asp Val Leu Ser Tyr His Ala Thr Cys Ser
130 130 135 140
133 Lys Ala Glu Val Asp Lys Phe Lys Ala Ala Asn Ile Pro Leu Val Ser
134 145 150 155 160
137 Glu Leu Ala Ile Asp Asp Ile His Phe Asp Asp Phe Ser Leu Asp Val
138 165 170 175
141 Asp Ala Met Ile Thr Ala Ala Leu Arg Met Phe Met Glu Leu Gly Met
142 180 185 190
145 Val Gln Lys Phe Lys Ile Asp Tyr Glu Thr Leu Cys Arg Trp Leu Leu
146 195 200 205
149 Thr Val Arg Lys Asn Tyr Arg Met Val Leu Tyr His Asn Trp Arg His
150 210 215 220
153 Ala Phe Asn Val Cys Gln Leu Met Phe Ala Met Leu Thr Thr Ala Gly
154 225 230 235 240
157 Phe Gln Asp Ile Leu Thr Glu Val Glu Ile Leu Ala Val Ile Val Gly
158 245 250 255
161 Cys Leu Cys His Asp Leu Asp His Arg Gly Thr Asn Asn Ala Phe Gln
162 260 265 270
165 Ala Lys Ser Gly Ser Ala Leu Ala Gln Leu Tyr Glu Thr Ser Ala Thr
166 275 280 285
169 Leu Glu His His His Phe Asn His Ala Val Met Ile Leu Gln Ser Glu

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173 Gly His Asn Ile Phe Ala Asn Leu Ser Ser Lys Glu Tyr Ser Asp Leu
174 305      310      315      320
177 Met Gln Leu Leu Lys Gln Ser Ile Leu Ala Thr Asp Leu Thr Leu Tyr
178      325      330      335
181 Phe Glu Arg Arg Thr Glu Phe Phe Glu Leu Val Ser Lys Gly Glu Tyr
182      340      345      350
185 Asp Thr Asn Ile Lys Asn His Arg Asp Ile Phe Arg Ser Met Leu Met
186      355      360      365
189 Thr Ala Cys Asp Leu Gly Ala Val Thr Lys Pro Trp Glu Ile Ser Arg
190      370      375      380
193 Gln Val Ala Glu Leu Val Thr Ser Glu Phe Phe Glu Gln Gly Asp Arg
194 385      390      395      400
197 Glu Arg Leu Glu Leu Lys Leu Thr Pro Ser Ala Ile Phe Asp Arg Asn
198      405      410      415
201 Arg Lys Asp Glu Leu Pro Arg Leu Gln Leu Glu Trp Ile Asp Ser Ile
202      420      425      430
205 Cys Met Pro Leu Tyr Gln Ala Leu Val Lys Val Asn Val Lys Leu Lys
206      435      440      445
209 Pro Met Leu Asp Ser Val Ala Thr Asn Arg Ser Lys Trp Glu Glu Leu
210      450      455      460
213 His Gln Lys Arg Leu Leu Ala Ser Thr Ala Ser Ser Ser Ser Pro Ala
214 465      470      475      480
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218      485      490
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222 <211> LENGTH: 19
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232 <212> TYPE: DNA
233 <213> ORGANISM: Homo sapiens
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240 <211> LENGTH: 30
241 <212> TYPE: DNA
242 <213> ORGANISM: Homo sapiens
244 <400> SEQUENCE: 5
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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date